

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of claims:**

1-121. (Canceled)

122. (Currently amended) An array, comprising:

a positionally-addressable ordered array of polynucleotide probes bound to a solid support; and

said polynucleotide probes comprising a ~~first~~ plurality of at least 100 polynucleotide probes of different nucleotide sequences, each said different nucleotide sequence comprising a sequence complementary and hybridizable to a different genomic sequence of the same species of organism, said respective genomic sequences ~~for~~ complementary and hybridizable to the probes being found at sequential sites in said genome of said species of organism, wherein the distance between 5' ends of said sequential sites is always less than 500 bp, wherein the genomic sequences ~~for~~ complementary and hybridizable to said ~~first~~ plurality of probes span a genomic region of at least 25,000 bp.

123-177. (Canceled)

178. (Withdrawn, Amended) A method for preparing an array comprising synthesizing a plurality of polynucleotide probes on a solid support, wherein:

said polynucleotide probes are ordered on said solid support so as to be positionally-addressable;

said polynucleotide probes comprise a plurality of at least 100 polynucleotide probes of different nucleotide sequences;

each said different nucleotide sequence comprises a sequence complementary and hybridizable to a different genomic sequence of the same species of organism;

said respective genomic sequences ~~for~~ complementary and hybridizable to said polynucleotide probes are found at sequential sites in the said genome of said species of organism;

the distance between 5' ends of said sequential sites is always less than 500 bp; and

the genomic sequences ~~for~~ complementary and hybridizable to said plurality of probes span a genomic region of at least 25,000 bp.

179-184. (Canceled)

185. (Currently amended) The array of claim 122, wherein regions of low information content selected from the group consisting of repetitive elements, simple repeats, ~~or~~ and polyX repeats have been excluded from said different nucleotide sequences.

186. (Currently amended) The array of claim 185, wherein the array has ~~in the range of~~ 150 to 1,000 different polynucleotide probes per 1 cm<sup>2</sup>.

187. (Currently amended) The array of claim 185, wherein the array has ~~in the range of~~ 1,000 to 10,000 different polynucleotide probes per 1 cm<sup>2</sup>.

188. (Currently amended) The array of claim 185, wherein the array has ~~in the range of~~ 10,000 to 50,000 different polynucleotide probes per 1 cm<sup>2</sup>.

189. (Previously presented) The array of claim 185, wherein the array has greater than 50,000 different polynucleotide probes per 1 cm<sup>2</sup>.

190. (Currently amended) The array of claim 185, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

191. (Currently amended) The array of claim 185, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

192. (Currently amended) The array of claim 185, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

193. (Previously presented) The array of claim 185, wherein the nucleotide sequences of the probes consist of no more than 1,000 nucleotides.

194. (Currently amended) The array of claim 193, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

195. (Currently amended) The array of claim 193, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

196. (Currently amended) The array of claim 193, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

197. (Currently amended) The array of claim 185, wherein the nucleotide sequences of the probes consist of ~~in the range of~~ 10-200 nucleotides.

198. (Currently amended) The array of claim 197, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

199. (Currently amended) The array of claim 197, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

200. (Currently amended) The array of claim 197, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

201. (Currently amended) The array of claim 185, wherein the nucleotide sequences of the probes consist of ~~in the range of~~ 10-30 nucleotides.

202. (Currently amended) The array of claim 201, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

203. (Currently amended) The array of claim 201, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

204. (Currently amended) The array of claim 201, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

205. (Previously presented) The array of claim 185, wherein the nucleotide sequences of the probes consist of ~~in the range of~~ 20-50 nucleotides.

206. (Currently amended) The array of claim 205, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

207. (Currently amended) The array of claim 205, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

208. (Currently amended) The array of claim 205, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

209. (Currently amended) The array of claim 185, wherein the nucleotide sequences of the probes consist of ~~in the range of~~ 40-80 nucleotides.

210. (Currently amended) The array of claim 209, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

211. (Currently amended) The array of claim 209, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

212. (Currently amended) The array of claim 209, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

213. (Currently amended) The array of claim 185, wherein the nucleotide sequences of the probes consist of ~~in the range of~~ 50-150 nucleotides.

214. (Currently amended) The array of claim 213, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

215. (Currently amended) The array of claim 213, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

216. (Currently amended) The array of claim 213, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

217. (Previously presented) The array of claim 185, wherein the nucleotide sequences of the probes consist of 60 nucleotides.

218. (Currently amended) The array of claim 217, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are overlapping in said genome.

219. (Currently amended) The array of claim 217, wherein said genomic sequences ~~for~~ complementary and hybridizable to the different probes are adjacent in said genome.

220. (Currently amended) The array of claim ~~456~~ 217, wherein said genomic sequence ~~for~~ complementary and hybridizable to each probe is spaced apart from that ~~for~~ complementary and hybridizable to other probes in said genome by less than 200 bp.

221. (Previously presented) The array of claim 185, wherein said organism is a eukaryote.

222. (Previously presented) The array of claim 185, wherein said organism is a human.

223. (Previously presented) The array of claim 185, wherein said organism is a plant.

224. (Previously presented) The array of claim 185, wherein said organism is a mammal.

225. (Currently amended) The array of claim 185, wherein said ~~first~~ plurality of polynucleotide probes is at least 1,000 probes.

226. (Currently amended) The array of claim 185, wherein said ~~first~~ plurality of polynucleotide probes is at least 10,000 probes.

227. (Currently amended) The array of claim 185, wherein said ~~first~~ plurality of polynucleotide probes is ~~in the range of~~ 1,000 to 50,000 probes.

228. (Currently amended) The array of claim 185, further comprising a sample on the surface of said solid support such that said sample (i) is in contact with said polynucleotide probes, and (ii) comprises ~~comprising~~ a population of cellular RNA or nucleic acid derived therefrom ~~on the surface of said solid support such that said sample is in contact with said polynucleotide probes, said contact being~~ under conditions conducive to hybridization between said population and said polynucleotide probes.

229. (Previously presented) The array of claim 228 wherein said population is labeled.

230. (Previously presented) The array of claim 228 wherein said population comprises total cellular mRNA or nucleic acid derived therefrom.

231. (Previously presented) The array of claim 228 wherein said population comprises nucleic acids of at least 10,000 different sequences.

232. (Currently amended) The array of claim 185, wherein the distance between said 5' ends of said sequential sites is determined after excluding consideration of said regions of low information content ~~repetitive elements, simple repeats, or polyX repeats.~~